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F006823; AAC51777.1; -
F005163; AAC29340.1; -
HGMIC627B; KCNK3.

3220; -
O; IPR003280; K-channel_2pore.
O; IPR001622; K-channel_pore.
O; IPR00636; M-channel_nlq.
O; IPR03032; TASK_channel.

F00520; Ion_trans; 1.
PRO1333; 2PORECHANNEL.

PRO1095; TASKCHANNEL.
channel; Transmembrane; Ion transport; Potassium transport;
olein.

M 1 8 CYTOPLASMIC (POTENTIAL).
M 9 29 POTENTIAL.
M 78 101 PORE FORMING 1 (POTENTIAL).
M 108 128 POTENTIAL.
M 129 158 CYTOPLASMIC (POTENTIAL).
M 159 179 POTENTIAL.
M 184 207 PORE FORMING 2 (POTENTIAL).
M 223 243 POTENTIAL.
D 244 394 CYTOPLASMIC (POTENTIAL).
D 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
E 394 AA; 43518 MW; 9FF4C8266F615FB7 CRC64;

h Similarity 100.0%; Score 2042; DB 1; Length 394;
94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MKRQNRVRLALIVCTTCTYLLGAAVFDALESEPELIERORLELQLQERARYNLSDQGYE 60
1 MKRQNRVRLALIVCTTCTYLLGAAVFDALESEPELIERORLELQLQERARYNLSDQGYE 60
1 ELERVVLRLKPHKAGVWRFGSFYFAITWTTGGHAMPSTDGKTCMFETALGIP 120
1 ELERVVLRLKPHKAGVWRFGSFYFAITWTTGGHAMPSTDGKTCMFETALGIP 120
1 TLPMFQSLGERINTLVYLHRAKKGIGRRADVSMMANVLFPGSCISTCIGAMASH 180
1 TLPMFQSLGERINTLVYLHRAKKGIGRRADVSMMANVLFPGSCISTCIGAMASH 180
1 YEHMTFOQNYCFTITTTIGDGVVLAQDKQALOTOPQVVAFSPVYLTGIVTAFLN 240
1 YEHMTFOQNYCFTITTTIGDGVVLAQDKQALOTOPQVVAFSPVYLTGIVTAFLN 240
1 LVVLERFMPNNADEKROEHRALTRNGQGGGGGGSAHTTDPASAAGGGFENY 300
1 LVVLERFMPNNADEKROEHRALTRNGQGGGGGGSAHTTDPASAAGGGFENY 300
1 FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT DOMAIN 184 207 PORE FORMING 2 (POTENTIAL).
FT TRANSMEM 223 243 POTENTIAL.
FT DOMAIN 244 411 CYTOPLASMIC (POTENTIAL).
FT CARBOHY 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 411 AA; 45276 MW; D2778016E09F2BF5 CRC64;

Query Match 90.6%; Score 1850.5; DB 1; Length 411;
Best Local Similarity 88.6%; 8; Mismatches 23; Indels 17;
Matches 363; Conservative 8; Mismatches 363; Indels 17;

P STANDARD; PRT; 411 AA.

1 SPANISH; PRT; 411 AA.

2001 (Rel. 40, Created)
2001 (Rel. 40, Last sequence update)
2001 (Rel. 40, Last annotation update)
Im channel subfamily K member 3 (Acid-sensitive potassium protein TASK) (TMK-related acid-sensitive K+ channel).
& TASK.
orvegicus (Rat).
a; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathli; Muridae; Murinae; F

OX NCBI_TaxId=10116;
RN [1]
RR SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=9809997; PubMed=9437008;
RA Leonoudakis D., Gray A.T., Winger B.D., Kindler C.H., Harada M
RA Taylor D.M., Chaves R.A., Forsythe J.R., Yost C.S.;
RT An open rectifier potassium channel with two pore domains in t
RT cloned from rat cerebellum;
RL J. Neurosci. 18:869-877 (1998).

- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POT CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTAS OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS 1 WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS 1 (BY SIMILARITY).
CC SUBCELLULAR LOCATION: Integral membrane protein (Potential)
CC TISSUE SPECIFICITY: STRONG EXPRESSION IN HEART. MODERATE EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY A
CC SKELETAL MUSCLE.
CC MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION. 21
CC BUPIVACAINE AND PHENYTOIN ACTIVATED BY PROTEIN KINASE A.
CC SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASS CHANNELS.
CC

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CC CC
CC EMBL; AR03184; AAC39525.1;
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003092; M+channel_nlq.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PRO1333; 2PORECHANNEL.
DR PRINTS; PRO1095; TASKCHANNEL.
DR K+channel; Transmembrane; Ion transport; Potassium transport
KW Glycoprotein.
FT DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 9 29 POTENTIAL.
FT DOMAIN 78 101 PORE FORMING 1 (POTENTIAL).
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FT DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
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FT CARBOHY 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL)
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OY 1 MKRQNRVRLALIVCTTCTYLLGAAVFDALESEPELIERORLELQLQERARYNL
Db 1 MKRQNRVRLALIVCTTCTYLLGAAVFDALESEPELIERORLELQLQERARYNL
OY 61 ELERVVLRLKPHKAGVWRFGSFYFAITWTTGGHAMPSTDGKTCMFETALGIP
Db 61 ELERVVLRLKPHKAGVWRFGSFYFAITWTTGGHAMPSTDGKTCMFETALGIP
OY 121 TLPMFQSLGERINTLVYLHRAKKGIGRRADVSMMANVLFPGSCISTCIG
Db 121 TLPMFQSLGERINTLVYLHRAKKGIGRRADVSMMANVLFPGSCISTCIG
OY 181 YEHMTFOQNYCFTITTTIGDGVVLAQDKQALOTOPQVVAFSPVYLTGIVTAFLV

